Volume 56(1) 75-92, 2012
Acta Biologica Szegediensis
http://www.sci.u-szeged.hu/ABS

Connection between sulfur metabolism and Hyn hydrogenase in *Thiocapsa roseopersicina* BBS

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The purple sulfur phototrophic bacterium, *Thiocapsa roseopersicina* BBS preferably utilizes sulfur compounds as electron donors and carbonate as inorganic carbon source for growth. Its sulfur metabolism is similar to that of *Allochromatium vinosum* but several variances could be recognized. *T. roseopersicina* contains several enzymatic routes for oxidation sulfur compounds, such as the modified Sox cycle which has an indispensable role in the assimilation thiosulfate, few sulfide oxidoreductases and the Dsr complex which is likely linked to sulfur oxidation. All these processes release electrons which – in principle - might be converted to H_2 via the hydrogenases and/or nitrogenase of the strain.

Hydrogenases are metalloenzymes capable of oxidation of molecular hydrogen and proton reduction. *Thiocapsa roseopersicina* BBS has four active NiFe hydrogenases. Hox1, Hox2 are cytoplasmic NAD^+ reducing hydrogenases, while the other two enzymes (Hyn, Hup) are bound to the membrane. The Hup and Hox1 hydrogenases are likely connected to the central quinone pool.

The main electron transport routes to/from the hydrogenases are not fully understood. In order to disclose these metabolic pathways, we cultivated single hydrogenase containing strains, in the presence of various kind of electron donors and the amounts of H_2 and various sulfur compounds were followed.

Hyn hydrogenase can produce hydrogen in the absence of carbonate. Under these conditions, sodium thiosulfate could promote hydrogen evolution, while the expression level of Hyn remained the same. Therefore, the elevated H_2 might be derived from the more intense metabolic flux. It was also shown that the oxidation of zero-valent sulfur can donate electrons to Hyn. Under these conditions, sulfur is an exclusive electron donor for both hydrogen evolution of Hyn and hydrogen sulfide formation which are consequently competitive processes. These results suggest that Hyn hydrogenase has a role in the elimination of extra electrons released from sulfur oxidation and protection against toxic effect of sulfide. Hydrogen evolution of Hyn hydrogenase was found only under illumination Moreover, the oxidation of various sulfur compounds was also blocked in darkness, therefore the light dependency of hydrogen evolution might be an indirect consequence of the light requirement of sulfur oxidation.

Glutathione amide forms were shown to be potential redox carrier in purple sulfur bacteria. Their role was investigated in the electron transport between sulfur metabolism and Hyn hydrogenase. In the absence of glutathione amide reductase there was an elevated hydrogen evolution by Hyn which indicated a competition between glutathione amide and Hyn hydrogenase for the electrons.

Oppositely, in the presence of elemental sulfur, hydrogen addition increased the Hyn mediated hydrogen sulfide formation, thus the connection between Hyn hydrogenase and sulfur metabolism was proved to be bidirectional. The Hyn dependent hydrogen sulfide formation was not light dependent. It was also pointed out that the two electron transport subunits of HynSL -Isp12- were indispensable in this linkage.

The interrelationship of hydrogen and sulfur metabolism was clearly demonstrated at physiological level. Based on these results, an integrated – but still hypothetical – electron transport model was outlined.

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The supramolecular organization of photosystem II in vivo studied by circular dichroism spectroscopy

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The light reactions of photosynthesis in higher plants take place in granal chloroplast thylakoid membranes, which contain chirally organized macrodomains composed of photosystem II (PSII) supercomplexes associated with light harvesting antenna complexes (LHCIIs). The physiological relevance of this hierarchic organization, which often manifest itself in semicrystalline macro-assemblies, has not been elucidated but the diversity of the supramolecular structures and their reorganizations under different conditions indicates its regulatory role. The present work focuses on the structural and functional roles of different components of LHCII-PSII supercomplexes. We used various growth conditions, influencing the protein composition, and different Arabidopsis mutants (koCP24, koCP26, koPsbW, koPsbX, dgd1), with altered organization of the membranes, and measured their circular dichroism (CD) spectra as well as their chlorophyll fluorescence kinetics to characterize the chiral macro-organization of the chromophores and the functional parameters of the membranes, respectively.

We have shown that the LHCII components play important roles in the macro-organisation of thylakoid membranes. We found that although these pigment-protein complexes themselves have only limited capacity to form ordered arrays in vivo, they can promote the